

What is claimed is:

1. A method for identifying the transcription binding motifs in the 5' regulatory region of a target gene or gene family that are responsible for gene regulation of said target gene or gene family in a particular cellular state, comprising:
 - a) selecting a target gene or gene family;
 - b) determining the number of appearances of transcription binding motif candidates in said 5' regulatory region of genes within said target gene family and experimentally determining the mRNA expression levels of other genes within said target gene family in said cellular state relative to genes not in said cellular state to obtain a first data set;
 - c) formulating a PROBE model of said data set; and
 - d) applying a singular value decomposition analysis and at least one more analysis selected from the group consisting of an Akaike information criterion test, a genetic algorithm, and a position specific scoring analysis, to said PROBE model, thereby identifying said transcription binding motifs responsible for gene regulation of said target gene or gene family in a particular cellular state.
2. The method of claim 1, wherein said gene family is selected from the group consisting of matrix metalloproteinases, cytokines, hormones, IL-1 responsive genes, cyclins, growth factor receptors, growth factors, oncogenes, and transcription factors.
3. The method of claim 1, wherein said 5' regulatory region comprises at least 300 base pairs.
4. The method of claim 1, wherein said 5' regulatory region comprises at least 500 bases.
5. The method of claim 1, wherein said target genes are interleukin-1 responsive genes and said cellular state is induced by contacting cells with interleukin-1.

6. The method of claim 1, wherein said target genes are present on a microarray.

7. The method of claim 1, comprising the step of:

5 e) linking said identified transcription factor binding motifs with at least one known transcription factor binding motifs.

8. The method of claim 7, wherein said at least one known transcription binding motifs are selected from the group consisting of AP1, AP2, NFY, PEA3, Sp1, TFIID, NF-kappa B, STAT, GATA-1, Oct-1, and TIE.

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9. The method of claim 1, comprising the step of:

e) experimentally confirming said identified transcription binding motifs by performing at least one analysis selected from the group consisting of Monte-Carlo simulation, promoter competition assay, gel shift assay, and mass spectrometry.

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10. The method of claim 9, comprising the step of:

f) linking the experimentally confirmed transcription factor binding motifs with at least one known transcription factor binding motifs.

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11. The method of claim 10, wherein said at least one known transcription binding motifs are selected from the group consisting of AP1, AP2, NFY, PEA3, Sp1, TFIID, NF-kappa B, STAT, GATA-1, Oct-1, and TIE.

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12. A method for predicting the expression levels of a target gene or gene family, comprising:

a) selecting a target gene or gene family;

b) determining the number of appearances of transcription binding motif candidates in said 5' regulatory region of genes within said target gene family and experimentally determining the mRNA expression levels of other genes within said target gene family to obtain a first data set;

30 c) formulating a PROBE model of said data set; and

d) applying a singular value decomposition analysis and at least one more analysis selected from the group consisting of an Akaike information criterion test, a genetic algorithm, and a position specific scoring analysis, to said PROBE model, thereby generating the estimated expression level of said target gene as a function of the weighed frequencies of the transcription binding motifs in the 5' regulatory region of said target gene.

13. The method of claim 12, wherein said gene family is selected from the group consisting of matrix metalloproteinases, cytokines, hormones, IL-1 responsive genes, cyclins, growth factor receptors, growth factors, oncogenes, and transcription factors.

14. The method of claim 12, wherein said 5' regulatory region comprises at least 300 base pairs.

15. The method of claim 12, wherein said 5' regulatory region comprises at least 500 bases.

16. The method of claim 12, wherein said target genes are present on a microarray.

17. The method of claim 12, comprising the step of:
e) linking said identified transcription factor binding motifs with at least one known transcription factor binding motifs.

18. The method of claim 17, wherein said at least one known transcription binding motifs are selected from the group consisting of AP1, AP2, NFY, PEA3, Sp1, TFIID, NF-kappa B, STAT, GATA-1, Oct-1, and TIE.

19. The method of claim 12, comprising the step of:
e) experimentally confirming said identified transcription binding motifs by performing at least one analysis selected from the group consisting of Monte-Carlo simulation, promoter competition assay, gel shift assay, and mass spectrometry.

20. The method of claim 19, comprising the step of:

f) linking the experimentally confirmed transcription factor binding motifs with at least one known transcription factor binding motifs.

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21. The method of claim 20, wherein said at least one known transcription binding motifs are selected from the group consisting of AP1, AP2, NFY, PEA3, Sp1, TFIID, NF-kappa B, STAT, GATA-1, Oct-1, and TIE.